CLAIM VERSION WITH MARKINGS TO SHOW CHANGES MADE

8. (Amended) An isolated nucleic acid comprising a nucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 1 [SEQ. ID. NO.: 1] or the amino acid sequence of SEQ ID NO: 1 [SEQ. ID. NO. :1] further comprising from 15 to 100 additional glutamine residues between amino acids 166 and 167.

9. (Amended) The isolated nucleic acid of claim 8, comprising the nucleotide sequence of SEQ ID NO: 1 [SEQ. ID. NO.: 1] from residue 49 to 3987 or comprising the nucleotide sequence of SEQ ID NO: 1 [SEQ. ID. NO.: 1] from residue 49 to 3987 and further comprising from 15 to 100 repeats of the sequence CAA or CAG between nucleotides 546 and 547.

10. (Amended) An isolated nucleic acid comprising a 2.5 kilobasepair Tsp E1 restriction fragment of human DNA that hybridizes to the nucleotide sequence of SEQ ID NO: 1 [SEQ. ID. NO.: 1] under conditions equivalent to 5 x SSC, 1 x Denhardt's solution, 10% sodium dodecyl sulfate, 20 mM sodium phosphate.

11. (Amended) An isolated nucleic acid comprising a 630 basepair Sma I-Apa I restriction fragment of human DNA that hybridizes to the nucleotide sequence of SEQ ID NO: 1 [SEQ. ID. NO.: 1] under conditions equivalent to 5 x SSC, 1 x Denhardt's solution, 10% sodium dodecyl sulfate, 20 mM sodium phosphate.

16. (Amended) A method for genetic screening for spinocerebellar ataxia type 2 comprising:

i) contacting a sample comprising nucleic acid obtained from a subject with a first oligonucleotide of at least 15 nucleotides that specifically hybridizes to [the complement of] SEQ ID NO: 1 [SEQ. ID. NO.: 1] between positions 4367 and 622 and with a second oligonucleotide of at least 15 nucleotides that specifically hybridizes to the complement of SEQ ID NO: 1 [SEQ. ID. NO.: 1] between nucleotides 1 and 543;

ii) performing a polymerase chain reaction using said sample nucleic acid as a template to obtain a product; and

iii) determining the length of said product;

wherein a finding of a length of said product indicating the presence of more than 35 triplets in the portion between nucleotides 544 and 622 indicates a predisposition to spinocerebellar ataxia type 2.

17. (Amended) The method of claim 16, wherein said first oligonucleotide comprises the nucleotide sequence of SEQ ID NO: 7 [SEQ. ID. NO. 7] or SEQ ID NO: 8 [SEQ. ID. NO. 8].

18. (Amended) The method of claim 16, wherein said second oligonucleotide comprises the nucleotide sequence of SEQ ID NO: 6 [SEQ. ID. NO. 6] or SEQ ID NO: 10 [SEQ. ID. NO. 10].